

Fig. 1

5' CGATCGTACGATCGATCGATC
 3' CGACCGATCGATCATCGTAGCTAGGCTCTAGGCATT 5'

3'-sequence of a primer perfectly matching a non-specific sequence amplified by other

5' CGATCGTACGATTCGATCAGAGCTCTCATGCTCGACG 3'
 3' AGCTAGGCTCTAGGCATTG

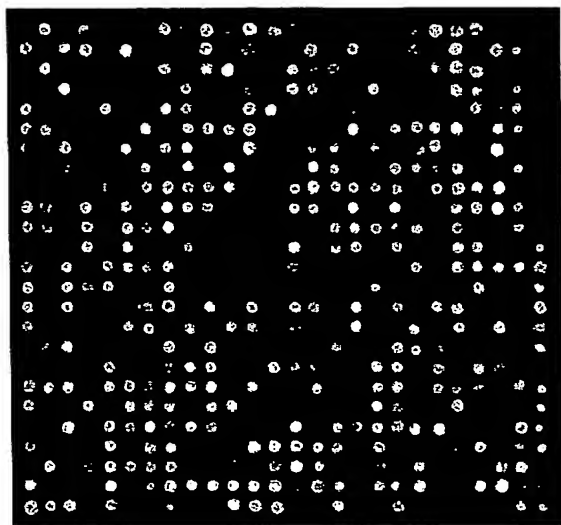
3'-sequence of a primer perfectly matching except one base
 with a non-specific sequence amplified by other primers

5' CGATCCGATCCGAGATCCGTAATCGATC 3'
 3' AGCTAGGCTCTATGCATCG

Maximal match between a primer sequence and a non-sequence amplified by other

Fig. 2

Red



Green

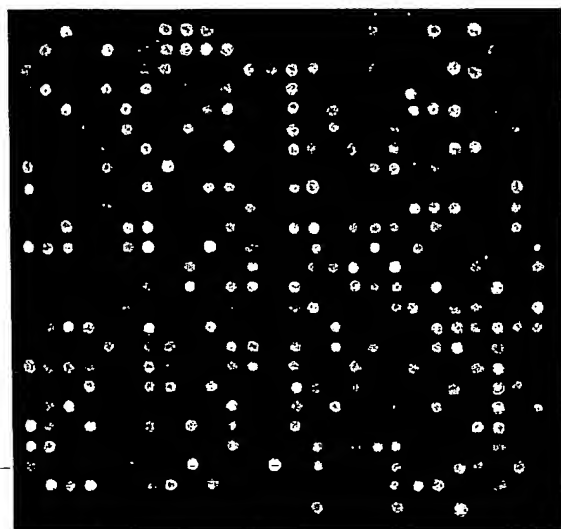


Fig. 3

Criteria Used in Designing Primers That Are Experimentally Acceptable	
T _m Range of the primers (°C)	75-103
Length of the primers (bp)	24-33
Number of consecutive matching bases between the 3' ends of any two primer molecules	<4
Number of consecutive matching bases with one mismatch between the 3'-ends of any two primer molecules	<7
Number of consecutive matching bases between the 3'-end of one primer molecule and anywhere in another primer molecule	<9
Number of consecutive matching bases with one mismatch between the 3'-end of one primer molecule and anywhere in another primer molecule	<11
Maximal number of matching bases between two primer molecules	<75%
Number of consecutive matching bases between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	12
Number of consecutive matching bases with one mismatch between the 3'-end of a primer molecule and anywhere in a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	15
Maximal number of matching bases between a primer molecule and a sequence of a PCR product that is not the sequence to which the primer is designed to anneal to	<80%

Fig. 4